

1/14

LOCUS Extrémité C-terminale récepteur AT2 160 BP DS-DNA

ORGANISM Souris

BASES 41 A 33 C 36 G 50 T

ac.nucléiques 1 TGTGTTAATC CCTTCCTGTA TTGTTTTGTT GGAAACCGCT
 TCCAACAGAA CGTCCGCAGT GTGTTTAGAG TTCCCATTAC
 TTGGCTCCAA GGCAAGAGAG AGACTATGTC TTGCAGAAAA
 121 GGCAGTTCTC TTAGAGAAAT GGACACCTTT GTGTCTTAAA

Traduction en acides aminés

CVNPFLYCFV GNRFAQNVRS VFRVPITWLQ GKRETMSCRK
 GSSLREMDTFVS•

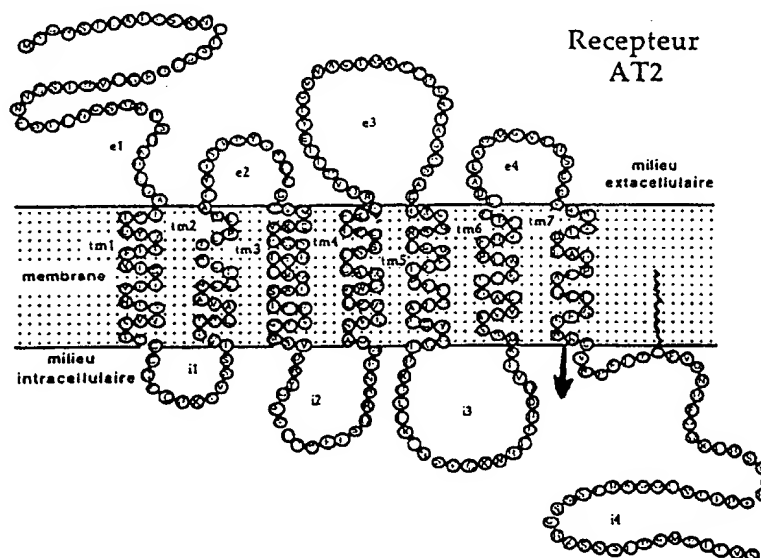


Figure 1

2/14

.... AGT AAC AAA GGT CAA AGA CAG TTG ACT GTA TCG
Codon 147

← Domain de liaison à l'ADN de GAL4 →

Site de	Smal	Sall
clonage	CCG GAA TTC CCG GGG ATC CGT CGA CCT...	
multiple	EcoRI	BamHI

Figure 2

3/14

GCTACCCCCCCCCACGCACCCCCCAATCTGGGTGGCCTGGCATTAGCATGTAAGCTTGTTTTCTCTGGC	71
TGTATCTCTTGGCCTGGAAGAACCCCGAGTTGCCAAGAGACACAGTATGTGATGGTCCCTGGAAAAGCTGCT	143
M L L S P K F S L	9
TCCCCTGCGAAGTTCTCCCACTGGCTTCGAAGAC ATG CTG TTG TCT CCC AAA TTC TCC TTA	204
S T I H V R L T A K G L L R N L R L	27
TCC ACC ATC CAC GTC CGC CTA ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT	258
P S G L R K N T V I F H T V E K G R	45
CCT TCG GGG CTC AGG AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG	312
Q K N P R S L C I Q T Q T A P D V L	63
CAG AAG AAT CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG	366
S S E R T L E L A Q Y K T K C E S Q	81
TCC TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC CAA	420
S G F I L H L R Q L L S R G N N K F	99
AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC AAC AAG TTT	474
E A L T V V I Q H L L S E R E E A L	117
GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG CGG GAG GAA GCA CTG	528
K Q H K T L S Q E L V S L R G E L V	135
AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC AGC CTC CGG GGA GAG CTA GTT	582
1 A A S S A C E K L E K A R A D L Q T	153
GCT GCT TCA AGC GCC TGT GAG AAG CTA GAA AAG GCT AGG GCT GAC TTA CAG ACA	636
A Y Q E F V Q K L N Q Q H Q T D R T	171
GCG TAT CAA GAA TTT GTC CAG AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG	690
E L E N R L K D L Y T A E C E K L Q	189
GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG	744
S I Y I E E A E K Y K T Q L Q E Q F	207
AGC ATT TAC ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT	798
D N L N A A H E T T K L E I E A S H	225
GAC AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC	852
2 S E K V E L L K K T Y E T S L S E I	243
TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT TCA GAA ATC	906
K K S H E M E K K S L E D L L N E K	261
AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG	960
Q E S L E K Q I N D L K S E N D A L	279
CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT GCT TTA	1014
3 N E R L K S E E Q K Q L S R E K A N	297
AAC GAA AGG TTG AAA TCA GAG GAG CAA AAG CAA CTG TCA AGA GAG AAG GCG AAT	1068
S K N P Q V M Y L E Q E L E S L K A	315
TCC AAA AAC CCT CAG GTC ATG TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT	1122

Figure 3.1

4/14

V	L	E	I	K	N	E	K	L	H	Q	Q	D	M	K	L	M	K	333	
GTG	TTA	GAG	ATC	AAG	AAT	GAG	AAG	CTG	CAC	CAG	CAG	GAC	ATG	AAG	CTA	ATG	AAG	1176	
M	E	K	L	V	D	N	N	T	A	L	V	D	K	L	K	R	F	351	
ATG	GAA	AAG	CTG	GTG	GAC	AAT	AAC	ACA	GCA	TTG	GTT	GAC	AAG	CTG	AAG	CGA	TTC	1230	
4	Q	Q	E	N	E	E	L	K	A	R	M	D	K	H	M	A	I	S	369
CAG	CAG	GAA	AAC	GAG	GAG	TTA	AAA	GCT	CGC	ATG	GAC	AAA	CAC	ATG	GCA	ATT	TCA	1284	
R	Q	L	S	T	E	Q	A	A	L	Q	E	S	L	E	K	E	S	387	
AGG	CAA	CTT	TCC	ACC	GAG	CAG	GCC	GCG	CTG	CAA	GAG	TCC	CTT	GAG	AAG	GAG	TCA	1338	
K	V	N	K	R	L	S	M	E	N	E	E	L	L	W	K	L	H	405	
AAG	GTC	AAC	AAG	AGA	CTG	TCC	ATG	GAG	AAC	GAG	GAA	CTT	CTG	TGG	AAA	CTG	CAC	1392	
N	G	D	L	C	S	P	K	R	S	P	T	S	S	A	I	P	F	423	
AAC	GGA	GAC	CTG	TGC	AGC	CCC	AAG	AGA	TCC	CCC	ACC	TCC	TCG	GCC	ATC	CCT	TTC	1446	
Q	S	P	R	N	S	G	S	F	S	S	P	S	I	S	P	R	*	440	
CAG	TCC	CCC	AGG	AAT	TCT	GGT	TCC	TTC	TCC	AGC	CCC	AGC	ATC	TCA	CCC	AGA	TGA	1500	
CGGCTTCTGAACGCAGGAGACTCTCTGAAGGCACTGAGGTGCGCTTCTGCAGGACTGACCCTCTCATGGGA																		1571	
ACTCGAGTTGCTGCGTTAGCTCTCTGGAATATCCCCAGGATATCGGGAGAGCAGCCGCCAACCGTATCAGC																		1642	
TACGTACGAATAGAGAGCTCCAATAGAAGACTTTTAACTTGGTCCAAAAGCCTCCTCCAAAACAGATTTC																		1713	
GGAAGTGAAGTGGACATAGTTGCACAAAGCACTTACGGAACGAGGGAACCTTGTTCTTTGCCTTCCTTCAC																		1784	
CTAAGCATAGGCTTTCCAG																		1803	

Figure 3.2

cagtgtgatgtggttcagagggcagcttcttagacctgcaggagggagattgtattcagaggaagagcatcatt	72
ttggcaacatctgaaagtgaacacggaagccagaaacacttgccagccctgggggatttttttcttctatg	144
cctctgtggtggaatgacatttgctgtgttaggcattcttctctgactgtatttcttggccttgaagagtac	216
tgagtttaaaaagacagtatgtgacagtcctatggaaattgcctcttctgtgaaatctcgccacctgctccga	288
agac ATG TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG	343
M L L S P K F S L S T I H I R L T	17
GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA AGC ACT	397
A K G L L R N L R L P S G F R R S T	35
GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT CGA AGC TTA TGT	451
V V F H T V E K S R Q K N P R S L C	53
ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT GAG AAA ACA CTT GAA TTG	505
I Q P Q T A P D A L P P E K T L E L	71
ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA AGT GGA TTT ATC CTG CAG CTC AAG	559
T Q Y K T K C E N Q S G F I L Q L K	89
CAG CTT CTT GCC TGT GGT AAT ACC AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG	613
Q L L A C G N T K F E A L T V V I Q	107
CAC CTG CTG TCT GAG CGG GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA	667
H L L S E R E E A L K Q H K T L S Q	125
1 GAA CTT GTT AAC CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA	721
E L V N L R G E L V T A S T T C E K	143
TTA GAA AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG	775
L E K A R N E L Q T V Y E A F V Q Q	161
CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC ACC AGG	829
H Q A E K T E R E N R L K E F Y T R	179
GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG AAG TAC AAA ATG	883
E Y E K L R D T Y I E E A E K Y K M	197
CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT GAA ACC TCT AAG TTG GAA	937
Q L Q E Q F D N L N A H E T S K L E	215
ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA TTG CTA AAG AAG GCC TAT GAA GCC	991
I E A S H S E K L E L L K K A Y E A	233
TCC CTT TCA GAA ATT AAG AAA GGC CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT	1045
S L S E I K K G H E I E K K S L E D	251
TTA CTT TCT GAG AAG CAG GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT	1099
L L S E K Q E S L E K Q I N D L K S	269
3 GAA AAT GAT GCT TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA	1153
E N D A L N E K L K S E E Q K R R A	287
AGA GAA AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA	1207
R E K A N L K N P Q I M Y L E Q E L	305

Figure 41

6/14

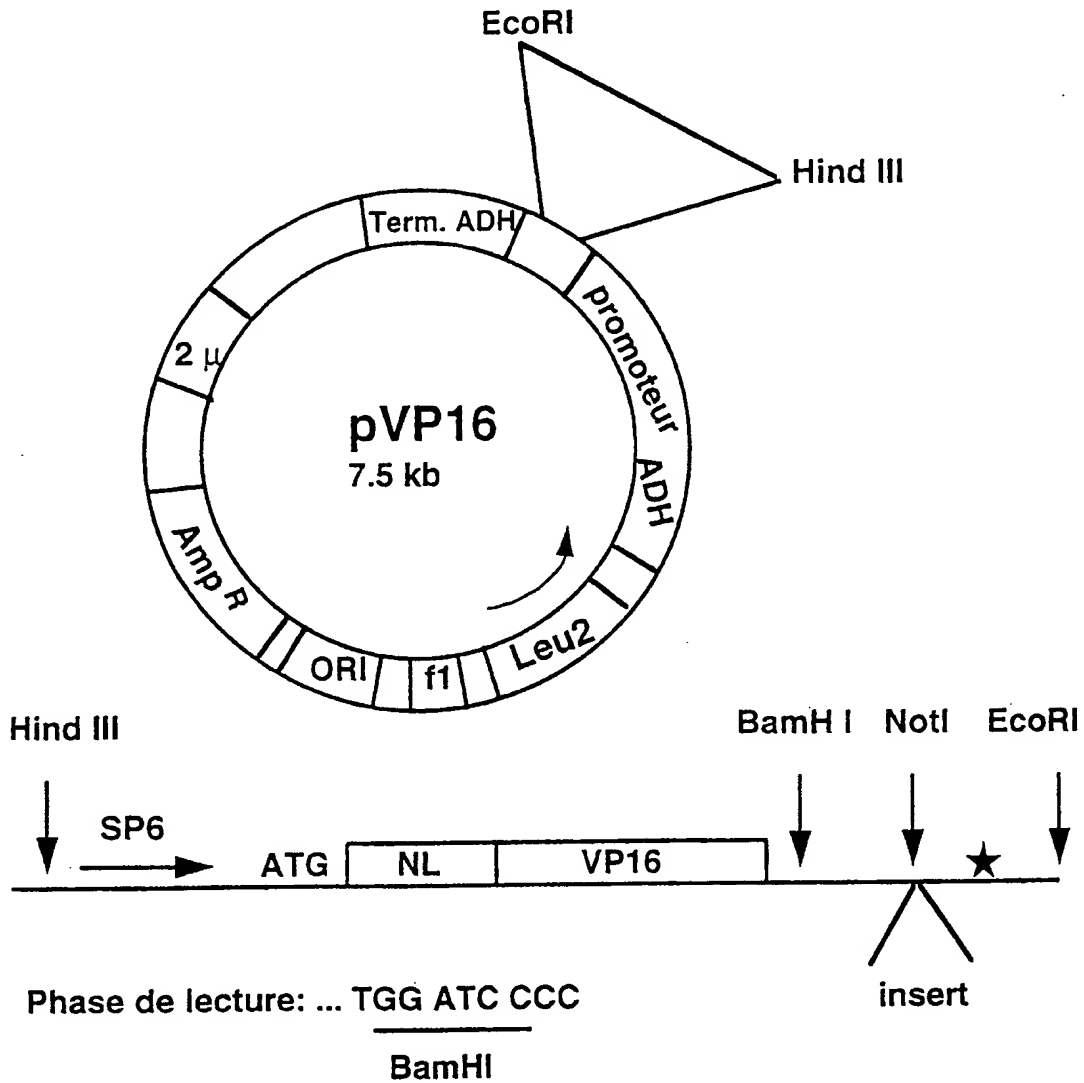
GAA AGC CTG AAA GCT GTG TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA CAG GAC 1261
 E S L K A V L E I K N E K L H Q Q D 323
 ATC AAG TTA ATG AAA ATG GAG AAA CTG GTG GAC AAC AAC ACA GCA TTG GTT GAC 1315
 I K L M K M E K L V D N N T A L V D 341
 AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG AAA GCT CGG ATG GAC AAG 1369
 K L K R F Q Q E N E E L K A R M D K 359
 CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG GAG CAG GCT GTT CTG CAA GAG TCG 1423
 H M A I S R Q L S T E Q A V L Q E S 377
 CTG GAG AAG GAG TCG AAA GTC AAC AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT 1477
 L E K E S K V N K R L S M E N E E L 395
 CTG TGG AAA CTG CAC AAT GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC 1531
 L W K L H N G D L C S P K R S P T S 413
 TCC GCC ATC CCT TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC 1585
 S A I P L Q S P R N S G S F P S P S 431
 ATT TCA CCC AGA TGA cacgtcccccaggtccacagactctctgaaagcattttgatgcaggtctgc 1651
 I S P R * 436
 aggactgaccccaaggaggaacgtgggcacaaagaggtatatcagcacacgtgtgatcaccttaggtaactgg 1723
 agcgtcaccaccggcggaatcgagcttctgagactggaagtctggaggaagacttttgcctccgtccaaaag 1795
 attcctccaaaaaaagattttaaaaaaagatttcggcatcgacacggacgttgttgacaaaagcacttaaaga 1867
 acgagagcatcttgttcattgcctttttcacctaagcataaggggaaaaactctcagggccctattaagatt 1939
 tataacctttgtaaatgttcttcaccacagacaccttcttgtgagttttcagttctgactgtgggggtgggggg 2011
 tgtgaatgaaatggatgtcacagagtgtcatgtgtctgatgcagcctcctctgctgtgtattaaatgtcaaa 2083
 atctgaatatatctggatatgtactaatcaataataatcaatcaatcagcatatacatatttcagccaaagcc 2155
 atagaagaaaaagcaatagttgcttgaattatgatcatctaccaccaactctgctcagccctgtaacaggggt 2227
 agggagaggggtataacaggaagagctttgacttgtccctgtctatacattctctgtatcttttgggggtaac 2299
 ttcttggcagtttttcagtggtcagccatgtcagttgaaactagatttttctgtagattttttacttacccta 2371
 tgtgagccctaactatcctgtaattcattttctcagggtatgtgtaaatgtagaaccctaatttttctata 2443
 aaaaaacaaactaactaactgtgttaaagaaagaaaaaggaagtaccaatgggtttttccaccttattttta 2515
 cctttgatctacccttgagatttaacctgtctcttccctccattattctcatttttcccttttacctttct 2587
 ccaccatccagagccacaaaagcaaaccttctacctcctacctaactttctctgggacaaggataaaggaat 2659
 atgattttccagagccccagagccagctcatctccagggtgtgaaaccactttccaaataaactaaagcct 2731
 ggatttgatattacaaattttgggaaatcttagaataaagaacgagaacaaggaagtcattggctagtataa 2803
 ttaagaaaggtaggattcagtgcttaccgatgatgcagtacttgatagaagaaaacagtcctgggaggatagc 2875
 gctcatttttcagttaccctttaaggagtccttcttcttgggaaagtagcagaatgggtccgcttctttcc 2947
 catgagtggaaaatgtggcttgtccaactctcctccaggttgcatctcagtttctttccaaaacttattacc 3019

Figure 4.2

ccccctaatacctgagactttggaaaaggtggaaggaagaactgttgctttatctccccctccctgcatgtgt 3091
caacattgtgatgtcagtatcttactaaatctacattcagtggtgtacaaataacagctgtagtaagaagaga 3163
ttcaggatgctagaggtgaatatttgggtcatttacatgtacactacatagcaagttgatactcatgttgca 3235
tggtcttttaaattagtgattttgtgtcttaagtctttaacttccaatacttcatcatgtatgtaaccttcc 3307
atgtttgcttctgataaatggaaatgtaggttcactgccacttcatgagatatctctgctcacgcttccaag 3379
ttgttctcaatgacattagccaaagtgggtttgccattcatccccctaggcatggtaaatcttgtgttggtc 3451
cctgctgtcctccgtattacgtgaccggcaataaatctcatagcagttaatataaaaacatcttctggaggat 3523
gggagagaaacaggaggggaagatgggaaacaaaatagagaattcttaagattttgtttaaaccaaatgtttca 3595
tgtagaatgcaaaatgttggcacgtcaaaaatatgaatgtgtagacaactgtagttgtggtcagtttgtagt 3667
gatgggaagtgtattttactctgatcaataaataatgctggaatactcaaaaaaaaaaaaaaaaaaaaaaa 3739
aaa 3742

Figure 4.3

8/14



★ codons de terminaison dans trois phases

pVP16 a été construit par Stan Hollenberg

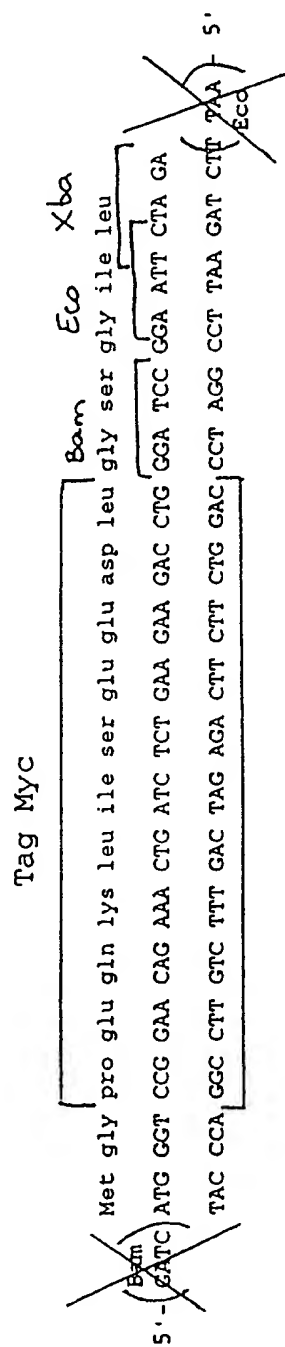
Figure 5

6 histidines

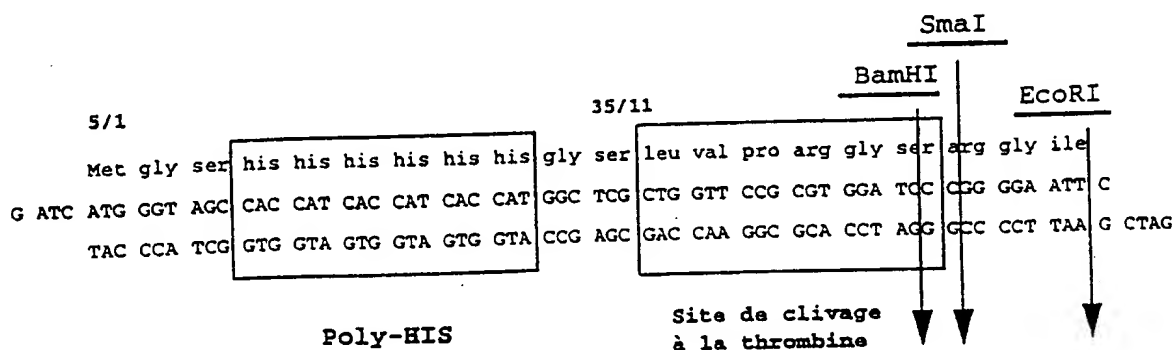
98.	<div style="border: 1px solid black; padding: 2px;">ATG</div> CGG GGT TCT CAT CAT CAT CAT CAT CAT GGT ATG
134	GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT
170	CTG TAC GAC GAT GAC GAT AAG GAT CGA TGG <u>GGA TCC</u> BamHI
206	GAG CTC GAG ATC TGC AGC TGG TAC CAT GGA ATT CGA
242	AGC TTG ATC CGG CTG CTA ACA AAG CCC GAA AGG AAG
278	CTG AGT TGG CTG CCA CCG CTG AGC AAT AAC TAG...

Figure 6

10/14

Figure 7

11/14



pBacPAK1-poly HIS -> Graphic Map

DNA sequence 5526 b.p. AACGGCTCCGCC ... TCATTAATGCAG circular

insertion polyHIS dans pBacpack en BamHI (CACCAT) 3 1270-1287

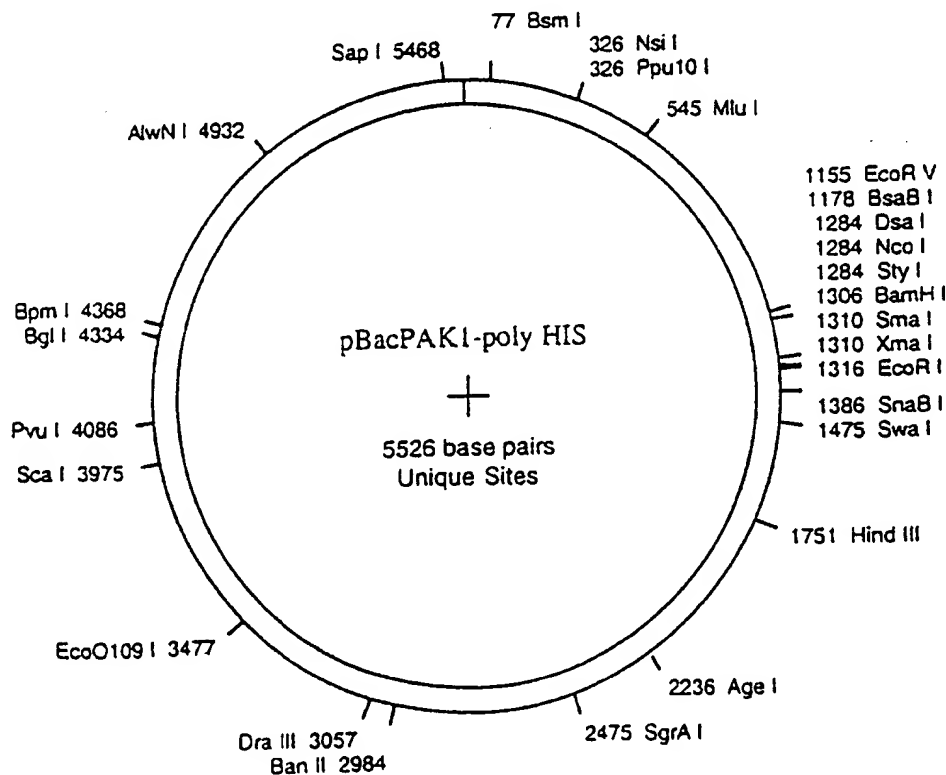
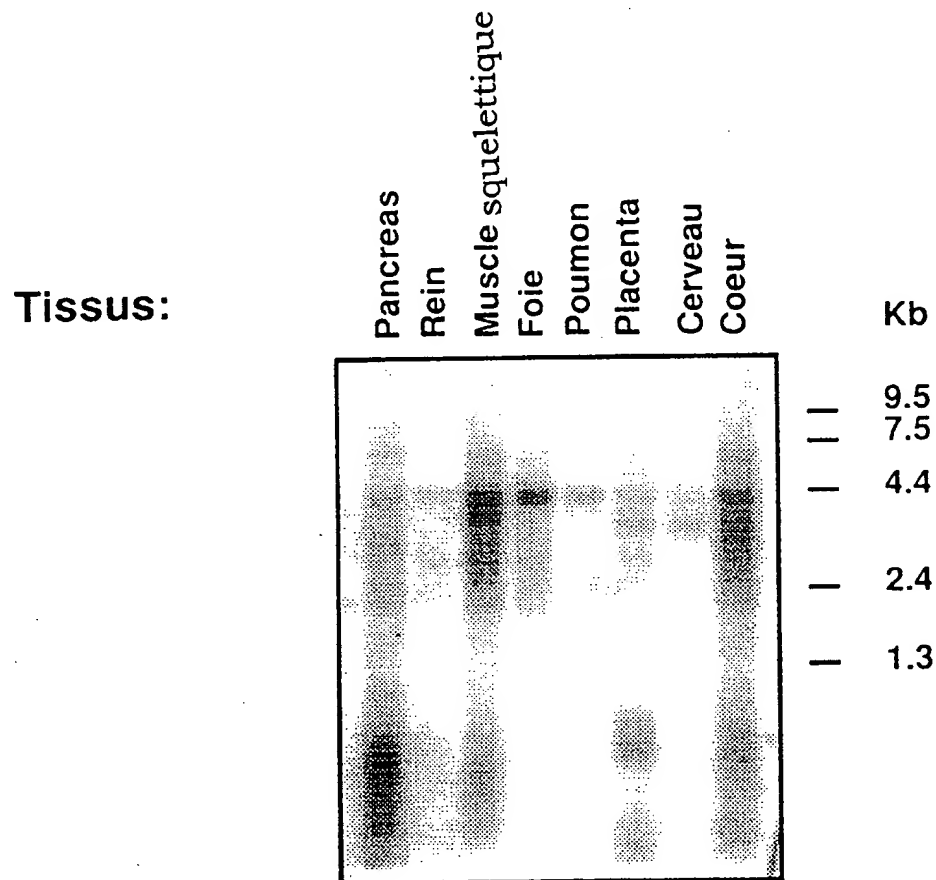


Figure 8

FEUILLE DE REMPLACEMENT (REGLE 26)

12/14

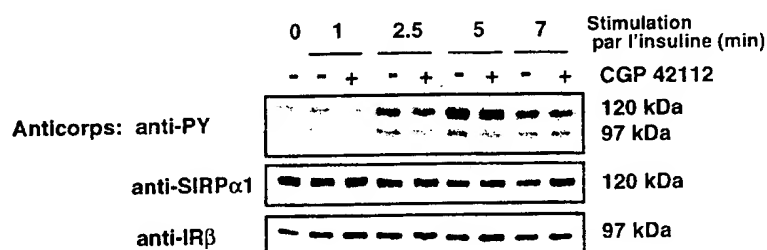
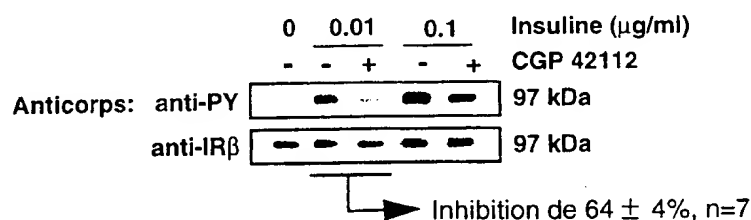
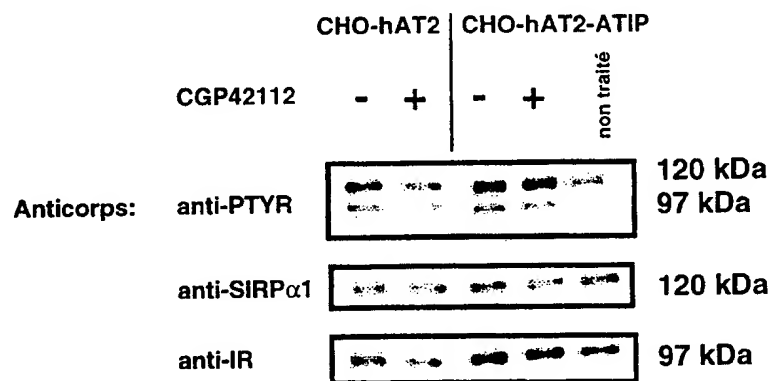
Figure 9

Surnageants :

	MBP-AT2	MBP _v	MBP-AT1	
Anticorps				
<u>anti-MBP</u>	—			← MBP-AT2
	48			
<u>anti-GST</u>	—			← GST-ATIP
	40			← GSTseul
	33			
Billes:	GST-ATIP	+	+	+
	GSTseul	—	—	—

Figure 10

14/14

CHO-hAT2**Colonne de lectine****CHO-hAT2 et CHO-hAT2-ATIP****Figure 11**